Entry of the following amendments and remarks is requested.

IN THE SPECIFICATION:

On page 9, lines 23 to 26 please replace the text with the following paragraph:

--For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al., *Protein* 28:405-420 (1997) [and http://www.psc.edu/general/ software/packages/pfam/pfam.html].--

On page 19, lines 6 to 22 please replace the text with the following paragraph:

--The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package [(available at http://www.gcg.com)], using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package [(available at http://www.gcg.com)], using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.--

On page 19 line 28 to page 20 line 12 please replace the text with the following paragraph:

--The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul et al., *J. Mol. Biol.* 215:403-10 (1990). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MEKK1 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MEKK1 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., *Nucleic Acids Res.* 25(17):3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. [See http://www.ncbi.nlm.nih.gov].--

IN THE CLAIMS:

Please cancel claims 27 - 52, without prejudice or disclaimer and add the following new claims (53 - 60) drawn to the subject matter of the Group I invention:

53. (New) An isolated nucleic acid selected from the group consisting of:

   a. a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3;

   b. a nucleic acid comprising the nucleotide sequence of the cDNA insert of the plasmid deposited with the ATCC as Accession Number PTA-1836 or a potion thereof, comprising the coding region;